

OFFICIAL

RECEIVED
CENTRAL FAX CENTER
JUN 16 2004Attorney Docket No: 23540-07445/US
Client Ref: 2001-072-2
USSN: 09/955,663

AMENDMENTS TO THE CLAIMS

1. (Currently amended): A method for estimating the precision of measurements taken from an array, comprising:

- (a) identifying a set of low-level data measurements;
- (b) estimating a standard deviation, σ_ϵ of an additive error component, ϵ ;
- (c) estimating a background parameter, α ;
- (d) identifying a set of replicated high-level data measurements;
- (e) estimating a standard deviation, σ_η , of a proportional error component, η from

the standard deviation of the logarithm of the replicated high-level data set;

(f) measuring a signal, y , wherein said signal indicates an amount of a biological molecule; and

- (g) estimating a variance of the measured signal as

$$\underline{Var\{y\} = \mu^2 e^{\sigma_\eta^2} (e^{\sigma_\eta^2} - 1) + \sigma_\epsilon^2}$$

wherein μ is the amount of the biological molecule and

$$\underline{y = \alpha + \mu e^\eta + \epsilon}$$

and wherein each model quantity is replaced by an estimate thereof.

$$\underline{Var(\hat{\mu}) = \hat{\sigma}_\epsilon^2 + \hat{\mu}^2 e^{\sigma_\eta^2} (e^{\sigma_\eta^2} - 1)}, \text{ where } \hat{\mu}^2 = (y - \alpha)^2$$

2. (Original): The method of claim 1, wherein said identifying step (a) comprises the use of a thresholding algorithm to establish a cutoff, and the set of low-level data consists of those data with values less than the cutoff.

3. (Currently amended): The method of claim 2, wherein the thresholding algorithm comprises the steps of:

- (a) identifying A_N , an initial set of low-level data measurements consisting of q percent of the total number of data points having the lowest measurement values, $A_N = \{x_1, x_2, \dots, x_{nq}\}$;
- (b) calculating a mean and a standard deviation of the initial set;

Attorney Docket No: 23540-07445/US
Client Ref: 2001-072-2
USSN: 09/955,663

- (c) calculating a cutoff point, u_N = mean plus $(c \times \text{the standard deviation})$ ~~ex the~~ standard deviation, wherein $2 \leq c \leq 3$;
- (d) defining a new set, $A_{N+1} = \{x_j < u_N\}$;
- (e) calculating a mean and standard deviation of the new set; and
- (f) repeating steps (c) and (d) using the mean and standard deviation of the new set until the algorithm converges.

4. (Currently amended): The method of claim 2, wherein the thresholding algorithm comprises the steps of:

- (a) identifying A_N , an initial set, of low-level data consisting of q percent of the total number of data points having the lowest measurement values, $A_N = \{x_1, x_2, \dots, x_{n_0}\}$;
- (b) calculating a median of the initial set, $m_0 = \text{median } \{x_j\}_{j=1}^{n_0}$ and a median of the absolute deviations about the median, $MAD_0 = \text{median } \{|x_j - m_0|\}_{j=1}^{n_0}$;
- (c) calculating a cutoff point, $u_0 = MAD_0 + (c \times s_0)$ ~~ex s₀~~, wherein $s_0 = MAD_0/0.675$ and $2 \leq c \leq 3$;
- (d) defining a new set, $A_{N+1} = \{x_j < u_N\}$;
- (e) calculating a median and a median of the absolute deviations about the median of the new set; and
- (f) repeating steps (c) and (d) using the median and the median of the absolute deviations about the median of the new set until the algorithm converges.

5. (Original): The method of claim 2, wherein the mean of the low-level data measurements is used as the estimate of the background parameter, α .

6. (Original): The method of claim 1, wherein the standard deviation of the low-level data measurements is used as the estimate of the parameter σ_e .

7. (Original): The method of claim 1, wherein, a mean of negative control data is used as the estimate of the background parameter, α .

8. (Original): The method of claim 1, wherein the biological molecule is a nucleic acid.

9. (Original): The method of claim 8, wherein the nucleic acid is mRNA.

10. (Original): The method of claim 8, wherein the biological molecule is DNA.

Attorney Docket No: 23540-07445/US
Client Ref: 2001-072-2
USSN: 09/955,663

11. (Original): The method of claim 10, wherein the DNA is cDNA.
12. (Original): The method of claim 10, wherein the DNA is genomic.
13. (Withdrawn): The method of claim 1, wherein the biological molecule is a protein.
14. (Withdrawn): The method of claim 1, wherein the biological molecule is a lipid.